	Search Text
1	galactose near2 oxidase
2	(galactose near2 oxidase) and (mutant or variant)
3	galactose near1 oxidase
4	(galactose near1 oxidase) and mutant
5	(galactose near1 oxidase) and varaint
6	((galactose near1 oxidase) and mutant) and "494"
7	((galactose near1 oxidase) and mutant) and enhanc
8	((galactose near1 oxidase) and mutant) and enhanced
9	((galactose near1 oxidase) and mutant) and DNA
10	(((galactose near1 oxidase) and mutant) and DNA) and substitution
11	((((galactose near1 oxidase) and mutant) and DNA) and substitution) and fusarium
12	"6498026"
13	galactose near1 oxidase
14	s (galactose near1 oxidase) and dendroides
15	(galactose near1 oxidase) and dendroides
16	((galactose near1 oxidase) and dendroides) and mutants
17	"6498026"
18	(galactose near1 oxidase) and mutant
19	"6498026"
20	galactose near2 oxidase
21	(galactose near2 oxidase) near10 dendroides
22	((galactose near2 oxidase) near10 dendroides) and (mutant or mutation or substitution or variant)
23	dactylium neral dendroides
24	galactose near1 oxidase
25	S72 or gao
26	S73 near10 S71
27	S74 and (mutant or modified or mutagenized or mutation or variant or variantion)
28	S75 and ("494" or "537")
29	S75 and ("413")
30	S73 and (mutant or modified or mutagenized or mutation or variant or variantion)
31	S78 and ("537" or "413" or "515" or "136")
32	S78 and n537d
33	"20040009561"
34	S81 and immobilized
35	S81 and lyophilization
36	S81 and racemate
37	S81 and homophenylalanine
38	S81 and fluoro

39	glucose near1 dehydrogenase

	Search Text
40	S87 near5 fusion
41	S87 near10 fusion
42	S87 and fusion
43	S87 and fusion
44	((glucose near1 dehydrogenase) and fusion)[AB]
45	S87 and (fusion near1 protein)

```
Database :        PIR_80:*
                  1:  pir1:*
                  2:  pir2:*
                  3:  pir3:*
                  4:  pir4:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                         SUMMARIES
                        %
Result                Query
   No.    Score   Match Length DB   ID                      Description
-----------------------------------------------------------------------------
     1    3420    99.9    728   1   A38084                  galactose oxidase
     2     275     8.0    504   2   D86332                  hypothetical prote
     3     270     7.9    547   2   T06758                  probable galactose
     4     266     7.8    545   2   T45935                  probable galactose
     5   258.5     7.5    650   2   AB2004                  hypothetical prote
     6   245.5     7.2    564   2   H86278                  F14L17.20 protein
     7     233     6.8    647   2   A45244                  exo-alpha-sialidas
     8     209     6.1   1014   1   NMCLSS                  exo-alpha-sialidas
     9     197     5.8   1361   2   T29435                  hypothetical prote
    10     197     5.8   2468   2   A83412                  hypothetical prote
    11   182.5     5.3    559   2   A48296                  glyoxal oxidase (E
    12     182     5.3   1441   2   B86807                  hypothetical prote
    13   167.5     4.9   5291   2   F90696                  hypothetical prote
    14   166.5     4.9   5188   2   B85547                  probable RTX famil
    15   163.5     4.8   2554   2   AB3528                  extracellular seri
    16     162     4.7    725   2   A90255                  hypothetical prote
    17     161     4.7   2232   2   T34434                  hypothetical prote
    18   159.5     4.7    856   2   T00349                  Avicelase III - As
    19   159.5     4.7   1433   2   T30261                  chitinase (EC 3.2.
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Database :        Issued_Patents_AA:*
                  1:  /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                  2:  /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                  3:  /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                  4:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  5:  /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                  6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3420	99.9	639	2	US-09-782-906-2	Sequence 2, Appli
2	3420	99.9	680	2	US-09-734-237B-77	Sequence 77, Appl
3	3420	99.9	681	2	US-09-734-237B-79	Sequence 79, Appl
4	3401	99.3	639	2	US-09-782-906-3	Sequence 3, Appli
5	3391	99.0	639	2	US-09-782-906-4	Sequence 4, Appli
6	3390	99.0	639	2	US-09-782-906-5	Sequence 5, Appli
7	2207	64.4	679	2	US-09-257-536-2	Sequence 2, Appli
8	2207	64.4	679	2	US-09-512-230-2	Sequence 2, Appli
9	466.5	13.6	850	2	US-09-902-540-12202	Sequence 12202, A
10	258	7.5	675	2	US-09-902-540-10824	Sequence 10824, A
11	244.5	7.1	492	2	US-09-902-540-16667	Sequence 16667, A
12	194	5.7	2736	2	US-09-252-991A-30227	Sequence 30227, A
13	170.5	5.0	1216	2	US-09-134-000C-5130	Sequence 5130, Ap
14	161	4.7	1752	2	US-09-865-621A-2	Sequence 2, Appli
15	150	4.4	1146	2	US-09-198-452A-580	Sequence 580, App
16	150	4.4	1749	2	US-09-640-419C-28	Sequence 28, Appl
17	149	4.4	1744	2	US-09-438-185A-542	Sequence 542, App